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Regional Guidelines for Sampling Douglas-fir Tussock Moth and Western Spruce Budworm

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Katharine A. Sheehan, Elizabeth A. Willhite, Andris Eglitis, Paul T. Flanagan, Tommy F. Gregg, and Bruce B. Hostetler

Forest Pest Management
USDA Forest Service
Pacific Northwest Region

These guidelines provide a sequence of steps for locating areas with increasing Douglas-fir tussock moth (DFTM) or western spruce budworm (WSB) populations and evaluating population trends. For additional information, contact Forest Pest Management at the Regional Office or Area Offices (Bend, La Grande, and Wenatchee).

Douglas-fir Tussock Moth

***Overview**:*

(1) monitor pheromone traps
|
if >40 moths/trap --> (2) delineate AU's, do lower crown larval sampling
|
if >2 larvae per 1000 sq.in. of midcrown foliage --> (3) refine AU boundaries

(1) Pheromone trapping

A network of DFTM pheromone trap plots has been established throughout susceptible forest types in Oregon and Washington. The purpose of this system of traps is to detect rising DFTM populations before significant defoliation occurs (Gregg and Twardus 1981). Early detection of increasing populations should provide enough time to analyze the situation to determine if suppression methods are warranted, and, if so, to allow insecticide application early in

the outbreak cycle. Average trap catches of 25 moths or more were thought to indicate that DFTM populations may be approaching the outbreak stage, and visible defoliation is likely within the next 2 years (Daterman et al. 1979, Gregg and Twardus 1981). This number was revised upward to 40 at a meeting of the Douglas-fir tussock moth technology transfer group in January, 1987. An average catch of 40 moths per trap is currently used as a threshold for initiating intensive larval population surveys the following spring.

a) Trap monitoring

Monitor the traps that are set out each year as part of the regional DFTM early warning system. Regional Office FPM will provide pheromone traps and instructions for handling the traps to participating Ranger Districts, state entomologists, and other cooperators. Cooperators are responsible for setting the traps out in late July, collecting them in October, and counting the DFTM moths found in the traps. Regional Office FPM is responsible for summarizing and reporting the results.

b) Sampling strategy

Conduct lower crown larval sampling the following spring in the vicinity of pheromone trap plots averaging 40 or more male moths per trap. In areas with plots averaging more than 25 but less than 40 moths per trap, either conduct cocoon sampling in the fall (to determine if larval sampling during the following spring is warranted) or set out additional plots during the following summer (to enhance the early warning system). We recommend the former approach if DFTM populations are increasing elsewhere in the Region or nine or more years have elapsed since the last outbreak. Pheromone traps should not be used to delineate analysis units; rather, they provide an index to population trends rather than an estimate of population levels.

(2) Lower crown larval sampling

After the system of pheromone traps has identified general areas where DFTM populations appear to be increasing, newly emerged larvae should be sampled during the following spring to monitor population trends within those areas. The first step in designing a plan for larval sampling and subsequent analyses is to identify specific areas, called "analysis units", where DFTM are thought to be increasing, and where the potential effects of an outbreak are expected to significantly affect forest management objectives.

(a) Delineating Analysis Units

Delineation of analysis unit boundaries is an important, fundamental step in the development of environmental analyses. Good analysis requires an accurate assessment of population levels and probable effects of an outbreak upon management objectives for resources in a specific area. Larger areas are more difficult and costly to sample and analyze than smaller areas. Analysis unit boundaries should be developed with careful consideration to include ***only*** *those areas where a DFTM outbreak would have unacceptable effects upon resource objectives.*

Timing

Ideally, analysis unit boundaries are identified before larval sampling is initiated in the spring. If that is not done, it is imperative to delineate analysis unit boundaries before fall cocoon sampling.

Procedure

Delineation of analysis units is a step-by-step procedure involving the screening of potential treatment areas through successive "filters" of qualifying criteria. The first step is to identify areas of host type. Host type stands are defined as those stands having 30 percent or more host crown cover. Major host species are Douglas-fir and true firs. Host typing should be based on existing stand composition, not the climax type. The next step is to ascertain those areas within the host type with resources which would be unacceptably affected by an outbreak of DFTM. Consider the management objectives identified in the forest plan. How will defoliation affect management goals and the desired future condition? Be site-specific. Include only those areas where the effects of defoliation upon resources would be unacceptable in terms of management goals and objectives. Other factors to consider when delineating analysis units include:

DFTM history -- DFTM outbreaks generally occur at 9-year intervals, though there is much variability to this general pattern (Shepherd et al. 1988). Historical records of the location of previous DFTM outbreaks in R6 have been summarized and mapped by L. Pettinger (Appendix A). Areas with no history of previous outbreaks still should be considered because some management practices (fire exclusion, selective logging of non-host species) may have increased the susceptibility of some stands to DFTM.

Site and stand conditions -- Conditions that increase stand susceptibility and/or vulnerability include: high proportion of host species (stand susceptibility increases as the proportion of host species increases), multiple canopy levels, high stocking levels, other stress factors (root disease, drought, other defoliators), low site productivity, and locations on ridgetops and steep upper slopes (Stoszek and Mika 1978).

On-the-ground observations -- When available, observations by trained personnel should also be considered.

(b) How to sample

Sample young larvae (first and second instars) on the lower crowns of host trees to estimate current and predicted population densities, classify population levels, and to identify plots that are candidates for cocoon sampling. The following sampling procedures were developed for western spruce budworm by Mason et al. (1989) and adjusted for DFTM based on the relation between lower crown and mid crown densities reported in Mason (1987). The recommended sample sizes (number of plots and number of trees per plot) are based on an analysis of pre-spray samples for eight plot-years (Appendix B).

Number and location of sample plots

Sample a minimum of 30 plots in each analysis unit. For analysis units larger than 30,000 acres, the plot density should be at least 3 plots per 1000 acres. Distribute plot locations so that the ranges of topographic and elevational differences within the analysis unit are represented.

Selecting sample trees and branches

Sample 5 trees at each plot. Sample trees must be either Douglas-firs or true firs that have current-year foliage within arm's reach, and must be at least 100 feet away from the nearest road. In all other respects, choose the sample trees at random. The outer 45 cm (18 in) of three branches (preferably from three different directions) from each tree should be sampled with a beating stick and cloth, and the total number of DFTM larvae from all three branches recorded.

When to sample

The optimum dates for sampling first and second instar DFTM larvae depend on local weather, specific site conditions (aspect, elevation, etc.), and host species. Host foliage development can be used as an indicator: early instar DFTM larvae usually should be sampled when new shoots are 50% elongated (2 to 3.5 cm [0.8 to 1.4 in] long), which generally occurs about 22 days after the first buds break (Wickman 1978). For planning purposes, first and second instar DFTM larvae generally can be sampled during late June. Sampling too early could result in a serious underestimation of DFTM populations if larval samples are taken before all eggs have hatched. If in doubt about timing, it is better to sample too late than too early. If foliage has not grown to the desired length in an area due to elevation or cool microsite, then delay sampling that area until later.

Data analysis

Analyze each analysis unit separately. We assume that one lower crown sample (from 3 branch tips) has 500 square inches of foliage, so multiply the average number of larvae found on 3 lower crown branch tips by 2 to get lower crown larval density per 1000 square inches. Multiply the lower crown density by 1.5 (or, if larval age/instar is known, by the ratio described in Scott and Mason [1992]) to determine the midcrown density (Mason 1987) and population status (Table 1). Those areas having populations predicted to reach suboutbreak or higher levels during the following spring are candidates for cocoon sampling.

Table 1. Population status for a range of DFTM larval densities on midcrown branches (taken from Mason 1977).

Population status	Relative abundance (% branches w/ larvae)	Larval density (no. / 1000 sq.in. foliage)
very low	rare, <2%	0 to 0.1
low	uncommon, 2-25%	0.1 to 2
suboutbreak	common, 25-50%	2 to 20
outbreak	abundant, >50%	20 or higher

(3) Cocoon sampling

The purpose of cocoon sampling is to continue monitoring populations and to refine analysis unit boundaries by further defining outbreak areas. Cocoon sampling generally is conducted in September for the purpose of predicting larval densities for the following spring. Mason et al. (1993) describe the lower crown cocoon sampling technique and recommend sample sizes for a range of cocoon densities and standard errors. To characterize the cocoon densities of large areas (such as analysis units), we recommend sampling more plots and fewer trees per plot than generally recommended by Mason et al. (1993), whose sample sizes were developed in large part for research purposes. Our recommended sample sizes (number of plots and number of trees per plot) were developed by starting with the sample sizes recommended for larvae (Appendix B), and then increasing those estimates somewhat arbitrarily to account for the more clumped distribution of pupae relative to larvae.

(a) How to sample

Ten plots should be sampled for cocoons for every 1,000 acres, with a minimum of 30 plots per analysis unit. Distribute plots as evenly as possible throughout the analysis unit. For each plot, choose 10 sample trees using the same guidelines described above for larvae. For each sample tree, examine the undersides of the outer 45 cm (18 in) of three different branches and record the total number of DFTM pupae or cocoons found.

(b) Data analysis

Data for each analysis unit identified in step 2(a) must be analyzed separately. Calculate the average cocoon densities in the lower crown, and then determine the predicted larval density and population status according to Table 2 (taken from Mason et al. 1993).

Table 2. Relation of estimated cocoon densities in preoutbreak populations of the DFTM to predicted larval densities and status in the next generation (taken from Mason et al. 1993).

Cocoon densities in lower crown (#/1000 sq.in.)	*Predicted larval midcrown densities (#/1000 sq.in.)*	*Predicted population status*
<0.01	*<2.0*	*low density; no defoliation*
0.01-0.30	*2.0-20.0*	*suboutbreak; little or no visible defoliation*
0.31-0.70	*21.0-40.0*	*moderate outbreak; defoliation visible on most host trees*
>0.70	*>40.0*	*severe outbreak; defoliation intense in upper crowns of many host trees with some trees completely defoliated*

Western Spruce Budworm

Overview:

(1) evaluate defoliation history

if 1+ year heavy
or 2+ yrs. moderate--> (2) delineate AU's,
do lower crown
larval sampling

if >8 larvae/tree ---> (3) deploy pheromone traps,
collect impact data,
refine AU boundaries

(1) Aerial detection of damage

Regional Office FPM conducts an annual aerial survey of most forested areas in Oregon and Washington. Monitor the resulting annual maps that indicate the location and severity of damage caused by WSB. Consider larval sampling only in those areas where at least two successive years of moderate defoliation (damage codes BS-2 or BS-M) have been recorded.

(2) Lower crown larval sampling

In areas where WSB defoliation has been observed for two or more years, sample older larvae (fourth and fifth instars) during the following spring to delineate specific outbreak areas more accurately, and to monitor existing damage and WSB population trends within those areas. The first step in designing a plan for larval sampling and subsequent analyses is to identify specific areas, called "analysis units", where WSB are thought to be increasing, and where the potential effects of an outbreak are expected to significantly affect forest management objectives.

(a) Delineating Analysis Units

Delineation of analysis unit boundaries is an important, fundamental step in the development of environmental analyses. Good analyses require an accurate assessment of population levels and probable effects of an outbreak upon management objectives for resources in a specific area. Larger areas are more difficult and costly to sample and analyze than smaller areas. Analysis unit boundaries, therefore, should be developed with careful consideration to include ***only*** *those areas where a WSB outbreak would have unacceptable effects upon resource objectives.*

Timing

Ideally, analysis unit boundaries are identified before larval sampling is initiated in the spring. If that is not done, it is imperative to

delineate analysis unit boundaries before pheromone traps are deployed in late June.

Procedure

Delineation of analysis units is a step-by-step procedure involving the screening of potential treatment areas through successive "filters" of qualifying criteria. The first step is to identify areas of host type. Host stands are defined as those stands having 30 percent or more host crown cover. Major host species are Douglas-fir, grand fir, white fir, subalpine fir, and Engelmann spruce. Host typing should be based on existing stand composition, not the climax type. The next step is to ascertain those areas within the host type with resources which would be unacceptably affected by an outbreak of WSB. Consider the management objectives identified in the forest plan. How will defoliation affect management goals and the desired future condition? Be site-specific. Include only those areas where the effects of defoliation upon resources would be unacceptable in terms of management goals and objectives. Other factors to consider when delineating analysis units include:

WSB history -- WSB outbreaks do not occur at regular intervals. Generally, several years of defoliation must occur before significant amounts of growth loss, topkill, or tree mortality are noted (Alfaro et al. 1982, Nichols 1988). Historical records of the location of previous WSB outbreaks in R6 from 1947 to 1979 have been summarized by Dolph (1980). Three general classes of outbreak frequency for the Pacific Northwest are described by Kemp et al. (1985). Areas with no history of previous outbreaks should still be considered because some management practices (fire exclusion, selective logging of non-host species) may have increased the susceptibility of some stands to WSB.

Site and stand conditions -- Conditions that increase stand susceptibility and/or vulnerability include: high proportions of host species (particularly when the hosts are the climax species for the site), multiple canopy levels, high stocking levels, other stress factors (root disease, drought, other defoliators, etc.), and shallow soil conditions such as are commonly found on ridgetops and steep slopes (Wulf and Cates 1987).

On-the-ground observations -- When available, observations by trained personnel should also be considered.

(b) How to sample

Sample older larvae (fourth and fifth instars) on the lower crowns of host trees to estimate current population density (Mason et al. 1989). Sample sizes may be tailored for an analysis unit if site-specific data (such as population samples from the previous year) are available; otherwise, use the recommended samples sizes which are based on 37 plot-years (Appendix B).

Number and location of sample plots

Sample a minimum of 30 plots for each analysis unit. For analysis units larger than 30,000 acres, the plot density should be at least 1 plot per 1000 acres. Distribute plot locations so that the ranges of topographic and elevational differences within the analysis unit are represented.

Selecting sample trees and branches

Sample 5 trees at each plot. Sample trees must be Douglas-firs or true firs that have current-year foliage within arm's reach, and are at least 100 feet away from the nearest road. In all other respects, choose the sample trees at random. Using a beating stick and cloth, sample the outer 45 cm (18 in) of three branches (preferably from three different directions) from each tree. Record the total number of WSB larvae from all three branches.

(c) When to sample

The optimum dates for sampling fourth and fifth instar WSB larvae depend on local weather, specific site conditions (aspect, elevation, etc.), and host species. The timing of host foliage development can be used as an indicator: these stages of WSB larvae usually can be sampled when new shoots are 50% elongated, i.e., 2 to 3.5 cm (0.8 to 1.4 in) long, which often occurs about 22 days after the first buds break (Wickman 1976, 1978). In most years, fourth and fifth instar WSB larvae can be sampled during mid to late June.

(d) Simultaneous sampling of DFTM and WSB larvae

DFTM and WSB populations may occur simultaneously in an area. When this occurs, it may be possible to sample first and second instar DFTM larvae and fourth, fifth, and sixth instar WSB larvae at the same time and on the same plot location (Wickman 1988). The optimal times for sampling DFTM and WSB larvae often do not coincide; in this situation, time sampling to coincide with first and second instar DFTM larval stages. Follow sampling procedures outlined above for DFTM and WSB larvae, and record the numbers of DFTM and of WSB larvae sampled from each tree.

(e) Data analysis

Data for each analysis unit must be analyzed separately. Calculate the average number of larvae found in 3 lower crown branches per tree. Eight larvae per tree is recommended as the threshold density that triggers additional population sampling (via pheromone traps) and damage estimates. Eight budworm larvae on three lower crown branches corresponds to 5.8 larvae per 18" midcrown branch (Torgersen et al. in press). We estimated that 6 larvae per 18" midcrown branch corresponds to approximately 5 larvae per 15" midcrown branch. Carolin and Coulter (1974) reported that larval densities of 3.49 to 6.69 (midpoint = 5.09) larvae per 15" midcrown branch results in moderate (26% to 50%) defoliation. We recommend that 8 larvae per 3-branch lower crown sample be used as the minimum threshold density because additional sampling is not warranted unless moderate (or higher) defoliation is expected.

(3) Pheromone Trapping and Impact Data

The purpose of pheromone trapping is to continue monitoring populations, predict subsequent-year defoliation levels, and to refine analysis unit boundaries by further defining outbreak areas. Tree impact data helps characterize current damage levels.

(a) Pheromone trapping

When 8 or more larvae are found per tree during lower crown beating, then use pheromone traps to continue evaluation of population levels. This phase of sampling consists of sampling adult WSB populations using traps baited with WSB pheromone. Place one trap at each larval sample plot in mid- to late-July. The traps may be collected after adult flight has occurred, usually by the first of August.

(b) Impact data

Collect tree impact data using the R6 modified stand exam method when traps are recovered from sample plots. This method involves establishing at each of the pheromone trap sites a variable radius plot for trees >2.9 inches in diameter at breast height (DBH), and a fixed radius plot for trees <3.0 inches in DBH. Information collected at these plots include site characteristics (slope, aspect, elevation, location, etc.) and tree characteristics (species, crown ratio, crown class, DBH, percent bare top, percent dead top, current defoliation, and cumulative defoliation).

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Appendix A: Historical Occurrence of DFTM

Figure 1 was developed by Leon Pettinger (R6 FPM) to summarize past records of defoliation by DFTM. He identified 3 zones:

Zone 1 -- A zone were defoliation by DFTM is most likely to occur. Changes in population trends are most likely to appear in this zone first.

Criteria for Zone 1:

* *a past history of defoliation by DFTM.*
* *Pheromone traps have caught more than 25 moths for 2 or more consecutive years, and subsequent larval surveys have found suboutbreak or higher populations of early instar larvae.*
* *Host type predominates and often is overstocked.*

Zone 2 -- A zone where visible defoliation by DFTM has never been recorded. Defoliation may occur here, but probably only after populations increase in Zone 1.

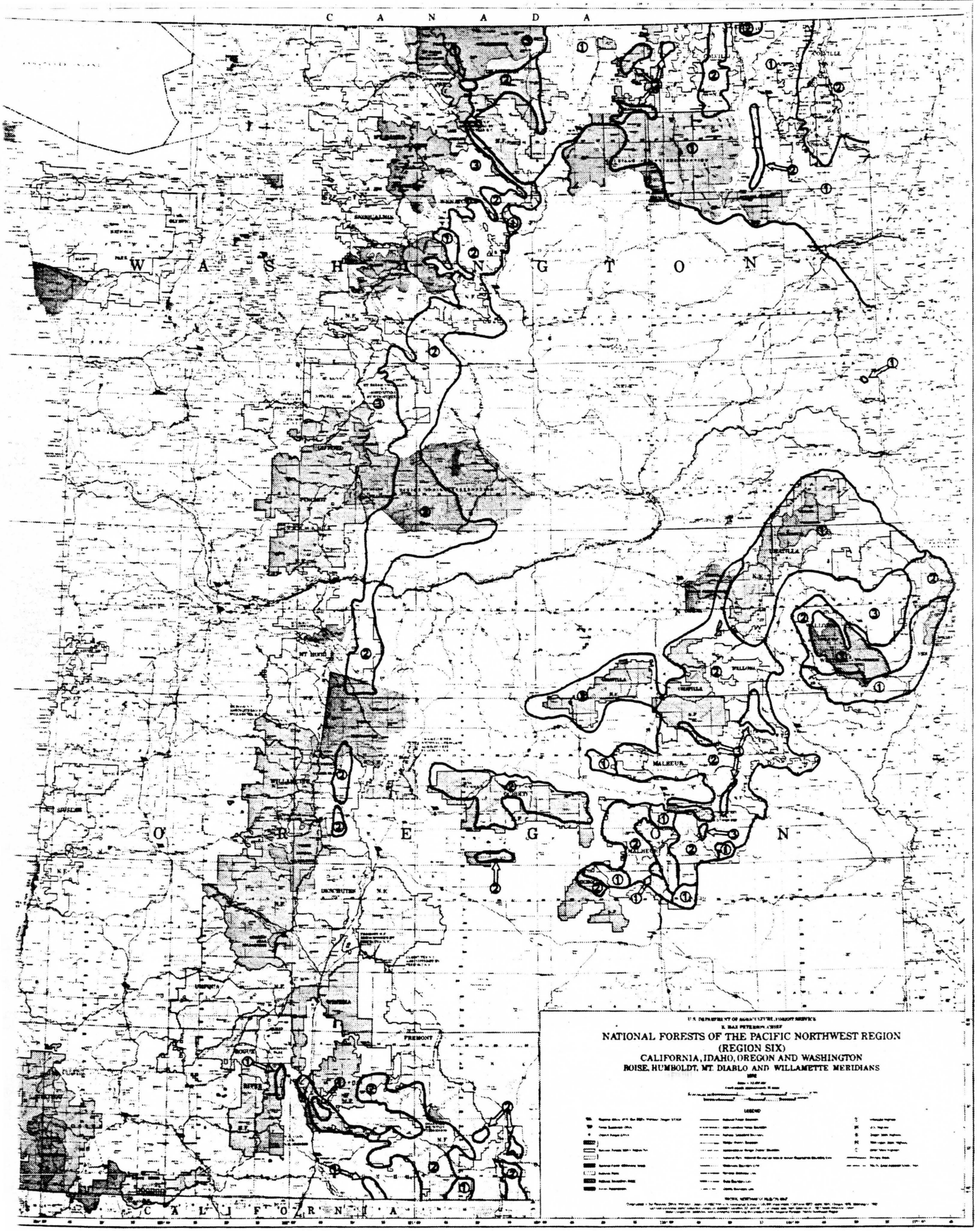
Criteria for Zone 2:

* *Pheromone traps only occasionally catch more than 25 moths.*
* *Early larval surveys consistently find low populations.*
* *Host type is common, and may or may not be overstocked.*
* *Zone 2 is sometimes more moist than Zone 1.*

Zone 3 -- A zone where outbreaks of DFTM are highly unlikely, and would be expected only when Zones 1 and 2 are fully involved in an outbreak.

Criteria for Zone 3:

* *Pheromone traps catch very few moths.*
* *Host type may or may not be common, overstocking is minimal.*
* *Non-host type.*
* *High elevation and moist forests.*
* *All west-side forests.*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Appendix B: Summary of Previous WSB and DFTM Multistage Samples

When designing sampling procedures for either western spruce budworm (WSB) or Douglas-fir tussock moth (DFTM) larvae, we must determine the number of plots and trees to be sampled. One option is to conduct a preliminary sample of the area in question and then use the observed mean population density and variation to calculate the optimum number of trees and plots to sample. However, this option is usually not feasible because of funding and time constraints. An alternative approach is to calculate the optimum sampling design for a large number of previous sampling efforts, and then summarize the results.

We examined 37 WSB samples and 9 DFTM samples taken from 1990 to 1992 in northeastern and central Oregon (Table B1). All populations were sampled using the lower crown beating technique (Mason 1987, Mason et al. 1989) during the early instar stage (DFTM) or late larval stage (WSB). These data sets were analyzed using the multistage sampling program MUST that was developed by Hazard and Stewart (1974) to determine the optimum number of plots and trees that should be sampled to obtain specified levels of precision with specific levels of probability.

Sample sizes were designed to minimize the cost of sampling, as measured in minutes. We assumed that one field crew would sample 10 plots on a typical field day, spending 1.5 hours to travel to the first plot, 20 minutes to travel between plots, and 1.5 hours to return from the last plot. We also assumed that one crew could use the lower crown beating technique to sample 5 trees on a plot in 15 minutes. These estimates were provided by Bruce B. Hostetler (R6-FPM), and reflect his experience in sampling both WSB and DFTM in the Blue Mountains of eastern Oregon during the late 1980s and early 1990s. The average travel time among plots is therefore 0.6 hours ((1.5 + 9.3333 + 1.5)/10) and the average time to sample one tree is 0.05 hours (3 minutes per tree), giving a cost ratio of 12:1 for plots:trees. Tables B2 and B3 summarize the number of trees per plot and number of plots that should be sampled to obtain estimates with a 0.90 probability of being within 20% or 30% of the standard error.*

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Table B1. Data sets used in this analysis.

insect	sample year	location	reason for sampling	area sampled (acres)	number of plots	trees per plot
DFTM	1991	Hells Canyon--WAW	pre-spray	35,717	39	5
		Catherine -- WAW	pre-spray	51,573	57	5
		Pine -- WAW	pre-spray	103,935	193	5
		Pine_check -- WAW	check area	---	31	5
DFTM	1992	Hells Canyon--WAW	follow up	35,717	30	5
		Catherine -- WAW	follow up	51,573	27	5
		Pine -- WAW	follow up	103,935	69	5
		Pine_check -- WAW	follow up	---	31	5
		Pine_dropped--WAW	follow up	---	28	5
WSB	1990	Jubilee	AU analysis	97,900	30	5
		Meacham	AU analysis	73,840	78	5
		Mill	AU analysis	100,100	30	5
		Thimbleberry	AU analysis	149,350	25	5
		LaGrande AU31	AU analysis	---	30	5
		LaGrande AU 4	AU analysis	6,165	25	5
		LaGrande AU 5	AU analysis	5,880	25	5
		LaGrande AU 6	AU analysis	6,540	25	5
		LaGrande AU 7	AU analysis	9,330	25	5
		LaGrande AU 8	AU analysis	5,367	25	5
		LaGrande AU 9	AU analysis	7,617	25	5
		LaGrande AU10	AU analysis	6,486	25	5
		LaGrande AU12	AU analysis	7,050	25	5
		LaGrande AU13	AU analysis	720	25	5
WSB	1991	Hells Canyon--WAW	pre-spray	35,717	39	5
		Catherine -- WAW	pre-spray	51,573	57	5
		Pine -- WAW	pre-spray	103,935	193	5
		Pine_check -- WAW	check area	---	31	5
WSB	1992	Hells Canyon--WAW	follow up	35,717	30	5
		Catherine -- WAW	follow up	51,573	27	5
		Pine -- WAW	follow up	103,935	69	5
		Pine_check -- WAW	follow up	---	31	5
		Pine_dropped--WAW	follow up	---	28	5
		DSIS.1 -- DES	AU analysis	24,149	40	10
		DSIS.2 -- WIL/DES	AU analysis	30,251	35	10
		DSIS.3 -- WIL/DES	AU analysis	22,474	30	10
		AU_1 -- MTH	AU analysis	---	59	10
		AU_2 -- MTH	AU analysis	---	30	10
		AU_3 -- MTH	AU analysis	---	15	10
		AU_4 -- MTH	AU analysis	---	30	10
		Indian	pre-spray	27,798	30	5
		Kuhn	pre-spray	57,093	34	5
		Meacham	pre-spray	41,788	29	5
		Mill	pre-spray	6,632	30	5
		Morgan	pre-spray	32,906	34	5
		Mt.Emily	pre-spray	32,539	31	5
		Thimbleberry	pre-spray	47,041	30	5

Table B2. Estimated optimum sample sizes for DFTM (probability = 0.90)

year	location	mean	SE - % of mean	# trees /plot	number of plots 30% SE	number of plots 20% SE	# plots / 1000 ac 30% SE	# plots / 1000 ac 20% SE
1991	Hells Canyon-WAW	3.01	34.7	4	148	332	4.1	9.3
	Catherine -- WAW	2.86	36.7	2	256	576	5.0	11.2
	Pine -- WAW	7.10	7.8	4	37	84	.36	.81
	Pine_check - WAW	13.74	11.7	9	10	22		
1992	Hells Canyon-WAW	0.39	30.9	5	86	194	2.4	5.4
	Catherine -- WAW	0.01	69.3	---[1]	---	---	---	---
	Pine -- WAW	0.56	26.4	3	154	347	1.5	3.3
	Pine_check - WAW	2.61	14.9	5	21	47		
	Pine_dropped-WAW	0.84	20.0	5	34	76		
	Average[2]	3.89	22.9	4.6	93.3	210	2.67	6.00

[1] *Population was too low to estimate optimum sample sizes.*

[2] *Does not include Catherine 1992.*

Table B3. Estimated optimum sample sizes for WSB (probability = 0.90).

year	location	mean	SE - % of mean	# trees /plot	number of plots		# plots / 1000 ac	
					30% SE	20% SE	30% SE	20% SE
1990	Jubilee	2.17	20.0	3	39	87	.40	.89
	Meacham	22.38	6.7	5	11	24	.15	.33
	Mill	0.69	18.8	6	30	67	.30	.67
	Thimbleberry	22.43	14.3	3	17	37	.11[1]	.25
	LaGrande AU31	18.72	16.5	2	28	62	---	---
	LaGrande AU 4	9.27	15.6	3	20	45	3.24	7.30
	LaGrande AU 5	2.69	11.6	5	10	23	1.70	3.91
	LaGrande AU 6	21.48	10.8	4	9	21	1.38	3.21
	LaGrande AU 7	29.09	8.8	5	6	13	.64	1.39
	LaGrande AU 8	10.69	11.8	3	12	26	2.24	4.84
	LaGrande AU 9	23.10	12.7	5	12	27	1.58	3.54
	LaGrande AU10	15.78	11.5	5	10	22	1.54	3.39
	LaGrande AU12	24.30	10.0	6	7	16	.99	2.27
	LaGrande AU13	28.31	10.4	4	9	20	12.50	27.78
1991	Hells Canyon-WAW	17.99	11.2	5	15	33	.42	.92
	Catherine -- WAW	29.79	8.6	3	14	32	.27	.62
	Pine -- WAW	14.83	6.4	3	26	58	.25	.56
	Pine_check - WAW	6.43	10.0	5	9	21	---	---
1992	Hells Canyon-WAW	11.97	11.2	4	12	27	.34	.76
	Catherine -- WAW	7.98	14.1	3	18	39	.35	.76
	Pine -- WAW	3.75	13.5	3	41	93	.39	.89
	Pine_check - WAW	1.80	20.8	2	45	102	---	---
	Pine_dropped-WAW	0.74	26.9	3	68	152	---	---
	DSIS.1 -- DES	13.30	7.7	7	8	18	.33	.75
	DSIS.2 -- WIL/DES	29.15	10.1	5	13	29	.43	.96
	DSIS.3 -- WIL/DES	23.11	12.4	3	17	38	.76	1.69
	AU_1 -- MTH	10.02	8.3	5	15	33	---	---
	AU_2 -- MTH	6.25	12.5	6	16	36	---	---
	AU_3 -- MTH	15.57	10.2	8	5	12	---	---
	AU_4 -- MTH	2.88	27.0	3	76	171	---	---

(continued on next page)

Table 3, continued:

year	location	mean	SE - % of mean	# trees /plot	number of plots 30% SE	number of plots 20% SE	# plots / 1000 ac 30% SE	# plots / 1000 ac 20% SE
1992	Indian Creek	11.63	11.0	4	12	26	.43	.94
	Kuhn	14.19	6.2	14	2	5	.035	.088
	Meacham	17.37	9.4	4	8	18	.19	.43
	Mill	26.93	9.3	4	8	18	1.21	2.71
	Morgan	10.93	17.6	4	33	75	1.00	2.28
	Mt. Emily	15.30	11.0	3	12	28	.37	.86
	Thimbleberry	19.85	6.5	5	4	9	.085	.19
	Averages							
AUs > 30,000ac (n=16)		15.05	11.6	4.6	18.4	41.3	.344	.716
AUs > 1,000ac (n=28)		16.15	11.4	4.5	15.2	34.1	.755	1.693
all AUs (n=37)		14.67	12.5	4.5	18.8	42.2	---	---

[1] *Size of the Analysis Unit (acres) is unknown.*